Amendments to the Specification:

Please replace the paragraph that begins on line 6 of page 90 with the following amended paragraph:

The mixture is then poured into a 5.0 x 20.0 cm Econo-Column (Bio-Rad, Laboratories, Hercules, CA), and the gel is washed with 30 column volumes of phosphate buffered saline (PBS). The unretained flow-through fraction is discarded. Once the absorbance of the effluent at 280 nM is less than 0.05, flow through the column is reduced to zero, and the anti-EE Sepharose gel is washed with 2.0 column volumes of PBS containing 0.2 mg/ml of EE peptide (AnaSpec, San Jose, CA). ~~The peptide that is used has the sequence GluTyrMetProValAsp~~. After 1.0 h at 4°C, flow is resumed and the eluted protein collected. This fraction is referred to as the peptide elution. The anti-EE Sepharose gel is then washed with 2.0 column volumes of 0.1 M glycine, pH 2.5, and the glycine wash is collected separately. The pH of the glycine-eluted fraction is adjusted to 7.0 by the addition of a small volume of 10X PBS and stored at 4°C for future analysis, if needed.

Please replace the title at line 5 of page 1 and at the first line of page 104 with the following amended title:

Polynucleotides Encoding Disintegrin Homologs, and Related Products

Please replace the abstract of the disclosure at page 104 with the following amended abstract:

ABSTRACT OF THE DISCLOSURE

The present invention relates to human polynucleotide and polypeptide molecules for zdint1, a novel member of the Disintegrin Proteases. The polypeptides, and polynucleotides encoding them, are believed to be cell-cell interaction modulating and may be used for delivery and therapeutics. The present invention also includes antibodies to the zdint1 polypeptides.

Please replace the paragraph that bridges page 84, line 32 to page 85, line 13 with the following amended paragraph:

Sequence tagged sites (STSs) can also be used independently for chromosomal localization. An STS is a DNA sequence that is unique in the human genome and can be used as a reference point for a particular chromosome or region of a chromosome. An STS is defined by a pair of oligonucleotide primers that are used in a polymerase chain reaction to specifically detect this site in the presence of all other genomic sequences. Since STSs are based solely on DNA sequence they can be completely described within an electronic database, for example, Database of Sequence Tagged Sites (dbSTS), GenBank, (National Center for Biological Information, National Institutes of Health, Bethesda, MD ~~http://www.ncbi.nlm.nih.gov~~), and can be searched with a gene sequence of interest for the mapping data contained within these short genomic landmark STS sequences.

Please replace the paragraph that starts at line 21 of page 93 with the following amended paragraph:

Zdint1 was mapped to chromosome 2 using the commercially available version of the "Stanford G3 Radiation Hybrid Mapping Panel" (Research Genetics, Inc., Huntsville, AL). The "Stanford G3 RH Panel" contains PCRable DNAs from each of 83 radiation hybrid clones of the whole human genome, plus two control DNAs (the RM donor and the A3 recipient). A publicly available WWW server ~~(http://shgc-www.stanford.edu)~~ allows chromosomal localization of markers.

Please replace the paragraph that starts at line 17 of page 94 with the following amended paragraph

The results showed linkage of Zdint1 to the framework marker SHGC-56733 with a LOD score of >12 and at a distance of 0 cR_10000 from the marker. The use of surrounding markers positions Zdint1 in the 2q33 region on the integrated LDB chromosome 2 map (The Genetic Location Database, University of Southhampton, WWW server~~: http://cedar.genetics. soton.ac.uk/public_html/~~).